

Amendments to th Specification:

Please replace the paragraph beginning at page 25, line 8, with the following rewritten paragraph:

--Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov>. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62---

Please replace the paragraph beginning on page 27, line 29, with the following paragraph:

--Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov>. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62---

Please replace the paragraph beginning on page 94, line 16, with the following paragraph:

--EXAMPLE 4: Isolation of cDNA Clones Encoding Human PRO243 by Genomic Walking

Introduction: Human thrombopoietin (THPO) is a glycosylated hormone of 352 amino acids consisting of two domains. The N-terminal domain, sharing 50% similarity to erythropoietin, is responsible for the biological activity. The C-terminal region is required for secretion. The gene for thrombopoietin (THPO) maps to human chromosome 3q27-q28 where the six exons of this gene span 7 kilobase pairs of genomic DNA (Gurney *et al.*, *Blood* 85: 981-988 (1995)). In order to determine whether there were any genes encoding THPO homologues located in close proximity to THPO, genomic DNA fragments from this region were identified and sequenced. Three P1 clones and one PAC clones (Genome Systems Inc., St. Louis, MO; cat. Nos. P1-2535 and PAC-6539) encompassing the THPO locus were isolated and a 140 kb region was sequenced using the ordered shotgun strategy (Chen *et al.*, *Genomics* U17:651-656 (1993)), coupled with a PCR-based gap filling approach. Analysis reveals that the region is gene-rich with four additional genes located very close to THPO: tumor necrosis factor-receptor type 1 associated protein 2 (TRAP2) and elongation initiation factor gamma (eIF4g), chloride channel 2 (CLCN2) and RNA polymerase II subunit hRPB17. While no THPO homolog was found in the region, four novel genes have been predicted by computer-assisted gene detection (GRAIL)(Xu *et al.*, *Gen. Engin. & Devel.* 16:241-253 (1994), the presence of CpG islands (Cross, S. and Bird, A., *Curr. Opin. Genet. & Devel.* 5: 109-314 (1995), and homology to known genes (as detected by WU-BLAST2.0)(Altschul and Gish, *Methods Enzymol.* 266:460-480 (1996)) (<http://blast.wustl.edu/blast/README.html>).--

Please replace the paragraph beginning on page 96, line 11, with the following paragraph:

Analysis: The identification and characterization of coding regions was carried out as follows: First, repetitive sequences were masked using RepeatMasker (A. F. A. Smit & P. Green, unpublished results http://ftp.genome.washington.edu/RM/RM_details.html) which screens DNA sequences in FASTA format against a library of repetitive elements and returns a masked query sequence. Repeats not masked were identified by comparing the sequence to the GenBank database using WUBLAST (Altschul, S & Gish, W., Methods Enzymol. 266: 460-480 (1996) and were masked manually.

Amendments to the Title:

Please replace the title with the following, as suggested by the Examiner:

PRO344 Protein

Amendments to the Abstract:

Please replace the abstract with the following:

The present invention is directed to a secreted polypeptide that inhibits neoplastic growth in tumor cells to secreted and transmembrane polypeptides and to nucleic acid molecules encoding these polypeptides. Also provided herein are vectors and host cells comprising these nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention, and to methods for producing the polypeptides of the present invention.